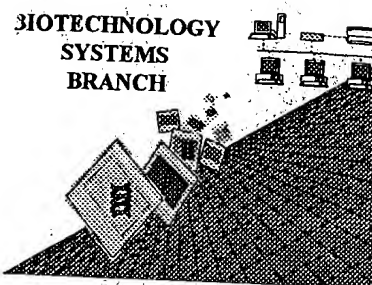


Y. J. Cal

Mailed on or about 9/27/99

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/009802A

Art Unit / Team No. : 1636

Date Processed by STIC: 9/13/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/009,802A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.
- 12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 3 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

UI: Yucel

1636

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

see
pp. 5, 2

Does Not Comply
Corrected Diskette Needed

```

1  <110> APPLICANT: McCarthy, Sean A.
2  <120> TITLE OF INVENTION: NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES
3      THEREFOR
4  <130> FILE REFERENCE: MEI-008
5  <140> CURRENT APPLICATION NUMBER: US/09/009,802A
6  <141> CURRENT FILING DATE: 1998-01-20
7  <150> EARLIER APPLICATION NUMBER: 08/842,898
8  <151> EARLIER FILING DATE: 1997-04-17
9  <150> EARLIER APPLICATION NUMBER: 60/071,589
10 <151> EARLIER FILING DATE: 1998-01-15
11 <160> NUMBER OF SEQ ID NOS: 19
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 2479
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (38)..(1087)
20 <400> SEQUENCE: 1
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22                                     Met Gln Arg Leu Gly Ala
23                                     1      5
24      acc ctg ctg tgc ctg ctg gcg gcg gcg gtc ccc acg gcc ccc gcg 103
25      Thr Leu Leu Cys Leu Leu Ala Ala Val Pro Thr Ala Pro Ala
26      10      15      20
27      ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151
28      Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
29      25      30      35
30      agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt 199
31      Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
32      40      45      50
33      gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa 247
34      Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
35      55      60      65      70
36      gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac 295
37      Glu Met Glu Ala Glu Glu Ala Ala Lys Ala Ser Ser Glu Val Asn
38      75      80      85
39      ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg 343
40      Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr
41      90      95      100
42      aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata 391
43      Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile
44      105      110      115

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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

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45      acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca 439
46      Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr
47      120                      125                      130
48      tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac 487
49      Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp
50      135                      140                      145                      150
51      gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac 535
52      Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr
53      155                      160                      165
54      acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt 583
55      Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser
56      170                      175                      180
57      gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg 631
58      Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met
59      185                      190                      195
60      gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc 679
61      Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys
62      200                      205                      210
63      cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg 727
64      Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val
65      215                      220                      225                      230
66      tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc 775
67      Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser
68      235                      240                      245
69      cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg 823
70      Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu
71      250                      255                      260
72      gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac 871
73      Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His
74      265                      270                      275
75      agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa 919
76      Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln
77      280                      285                      290
78      gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt 967
79      Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val
80      295                      300                      305                      310
81      ggc agc ttc atg gag gag gtg cgc cag gag ctg gag gac ctg gag agg 1015
82      Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg
83      315                      320                      325
84      agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct 1063
85      Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala
86      330                      335                      340
87      gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggtagatgtg 1117
88      Ala Leu Gly Arg Glu Glu Ile
89      345                      350
90      caatagaaat agctaattta tttccccagg tgtgtgtttt aagcgtgggc tgaccaggct 1177
91      tcttctctaca tcttcttccc agtaagtttc ccctctggtt tgacagcatg aggtgttgtg 1237
92      catttggtca gctccccagc gctgtttctcc aggtttcaca gtctggtgct tgggagagtc 1297
93      aggcagggtt aaactgcagg agcagtttgc caccctgtc cagattattg gctgctttgc 1357
94      ctctaccagt tggcagacag ccgtttgttc tacatggctt tgataattgt ttgaggggag 1417

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W-->

see item 10 on Error Summary sheet

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802A

 DATE: 09/13/1999
 TIME: 12:48:44

Input Set: I009802A.RAW

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95 gagatggaaa caatgtggag tctccctctg attggttttg gggaaatgtg gagaagagt 1477
96 ccctgctttg caaacatcaa cctggcaaaa atgcaacaaa tgaattttcc acgcagttct 1537
97 ttccatgggc ataggttaagc tgtgccttca gctgttgagc atgaaatgtt ctgttcaccc 1597
98 tgcattacat gtgtttattc atccagcagt gttgtcagc tctacctct gtgccagggc 1657
99 agcattttca tatccaagat caattccctc tctcagcaca gcctggggag ggggtcattg 1717
100 ttctcctcgt ccatcagggg tttcagagggc tcagagactg caagctgctt gcccaagtca 1777
101 cacagctagt gaagaccaga gcagtttcat ctggttgtag ctctaagctc agtgcctctc 1837
102 ccactacccc acaccagcct tgggtgccacc aaaagtgtct cccaaaagga aggagaatgg 1897
103 gatttttctt ttgagggcatg cacatctgga attaaggtea aactaattct cacatccctc 1957
104 taaaagtaaa ctactgttag gaacagcagt gttctcacag tgtggggcag ccgtccttct 2017
105 aatgaagaca atgatattga cactgtccct ctttggcagt tgcattagta actttgaaag 2077
106 gtatatgact gagcgttagca tacagggttaa cctgcagaaa cagtacttag gtaattgtag 2137
107 ggcgaggatt ataaatgaaa ttgcaaaat cacttagcag caactgaaga caattatcaa 2197
108 ccacgtggag aaaatcaaac cgagcagggc tgtgtgaaac atggttgtaa tatgcgactg 2257
109 cgaacactga actctacgcc actccacaaa tgatgttttc aggtgtcatg gactgttgcc 2317
110 accatgtatt catccagagt tcttaaagtt taaagttgca catgattgta taagcatgct 2377
111 ttctttgagt tttaaattat gtataaacat aagttgcatt tagaaatcaa gcataaatca 2437
112 cttcaactgc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2479

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<210> SEQ ID NO 2

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

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119      1           5           10           15
120 Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
121           20           25           30
122 Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
123           35           40           45
124 Glu Met Phe Arg Glu Val Glu Leu Met Glu Asp Thr Gln His Lys
125           50           55           60
126 Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
127           65           70           75           80
128 Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
129           85           90           95
130 Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
131           100          105          110
132 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
133           115          120          125
134 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
135           130          135          140
136 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
137           145          150          155          160
138 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
139           165          170          175
140 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
141           180          185          190
142 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
143           195          200          205
144 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg

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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/009,802A

 DATE: 09/13/1999
 TIME: 12:48:44

Input Set: I009802A.RAW

```

145          210          215          220
146      Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
147          225          230          235          240
148      Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
149          245          250          255
150      Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
151          260          265          270
152      Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
153          275          280          285
154      Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
155          290          295          300
156      Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
157          305          310          315          320
158      Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
159          325          330          335
160      Pro Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
161          340          345          350
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163 <211> LENGTH: 1050
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(1050)
169 <400> SEQUENCE: 3
170      atg cag cgg ctt ggg gcc acc ctg ctg tgc ctg ctg ctg gcg gcg gcg 48
171      Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
172      1 5 10 15
173      gtc ccc acg gcc ccc gcg ccc gct ccg acg gcg acc tcg gct cca gtc 96
174      Val Pro Thr Ala Pro Ala Pro Ala Thr Ala Thr Ser Ala Pro Val
175      20 25 30
176      aag ccc gcc ccg gct ctc agc tac ccg cag gag gag gcc acc ctc aat 144
177      Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
178      35 40 45
179      gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa 192
180      Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
181      50 55 60
182      ttg cgc agc gcg gtg gaa gag atg gag gca gaa gaa gct gct gct aaa 240
183      Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
184      65 70 75 80
185      gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat 288
186      Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
187      85 90 95
188      gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac 336
189      Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
190      100 105 110
191      cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt 384
192      Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
193      115 120 125
194      tca gag aca gtt atc aca tct gtg gga gac gaa gaa ggc aga agg agc 432

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PAGE: 5

RAW SEQUENCE LISTING PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999

TIME: 12:48:44

Input Set: I009802A.RAW

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195      Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
196          130                      135                      140
197      cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag      480
198      His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
199          145                      150                      155                      160
200      ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg      528
201      Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
202          165                      170                      175
203      ctc tgc acc cgg gac agt gag tgc tgt gga gac cag ctg tgt gtc tgg      576
204      Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
205          180                      185                      190
206      ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt      624
207      Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
208          195                      200                      205
209      gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga      672
210      Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
211          210                      215                      220
212      ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt      720
213      Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
214          225                      230                      235                      240
215      tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta      768
216      Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
217          245                      250                      255
218      gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc      816
219      Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
220          260                      265                      270
221      tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc      864
222      Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
223          275                      280                      285
224      gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc      912
225      Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
226          290                      295                      300
227      ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag      960
228      Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
229          305                      310                      315                      320
230      ctg gag gac ctg gag agg agc ctg act gaa gag atg gcg ctg agg gag      1008
231      Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
232          325                      330                      335
233      cct gcg gct gcc gcc gct gca ctg ctg gga agg gaa gag att      1050
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235          340                      345                      350
236      <210> SEQ ID NO 4
237      <211> LENGTH: 848
238      <212> TYPE: DNA
239      <213> ORGANISM: Homo sapiens
240      <220> FEATURE:
241      <221> NAME/KEY: CDS
242      <222> LOCATION: (125)..(796)
243      <400> SEQUENCE: 4
244      gaattcggca cgagagacga cgtgctgagc tgccagctta gtggaagctc tgctctgggt 60

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

↓ FYI

VERIFICATION SUMMARY
PATENT APPLICATION US/09/009,802A

DATE: 09/13/1999
TIME: 12:48:44

Input Set: I009802A.RAW

Line ? Error/Warning

Original Text

90 W "N" or "Xaa" used: Feature required
442 W "N" or "Xaa" used: Feature required
587 W Invalid/Missing Amino Acid Numbering

caatagaaat agctaattta tttcccccang tgtgtgct
accccattnn attctagagt cnagaacgca aggatctc